REMARKS

This paper is presented in response to the non-final official action dated January 23, 2009, wherein (a) claims 1 and 8-20 were pending, (b) claims 1, 8-12, and 14-17 were rejected under 35 U.S.C. § 112, 1st paragraph, for allegedly failing to comply with the written description requirement; (d) claims 11 and 12 were rejected under 35 U.S.C. § 112, 2nd paragraph, for allegedly failing to comply with the enablement requirement; and (d) claims 13 and 18-20 were rejected under 35 U.S.C. § 102(b) as being anticipated by Morris WO 03/039484 ("Morris").

With this paper, claims 11 and 12 have been canceled, and claims 1, 8, 13, and 17-19 have been amended. This paper is timely-filed, as it is accompanied by a petition for an automatic extension of time of one month and concurrent payment of the required fee. Reconsideration of the application, as amended, is solicited.

Claim 1 has been amended to recite that the sequence identity of the claimed nucleic acid is at least 90% of SEQ ID NO: 1 or 2. Support for this amendment can be found in the specification at page 5, line 10, for example. Claim 13 has been amended to include SEQ ID NO: 4 in the Markush structure, as the Patent Office has performed a search of this sequence and indicated it was free of the art. SEQ ID NO: 4 was originally restricted out in a restriction requirement dated June 21, 2007, but seems to have been inherently rejoined during prosecution of the elected species of SEQ ID NO: 1 and 2. Claims 1, 8, 13, and 17-19 have been amended, or further amended, as suggested by the examiner in the official action to clarify the sequence identity language. It is submitted that no new matter is presented with these amendments. Thus, claims 1, 8-10, and 13-20 are pending.

THE REJECTION OF CLAIMS 1, 8-10, AND 14-17 UNDER 35 USC § 112 SHOULD BE WITHDRAWN

Claims 1, 8-10, and 14-17 stand rejected under 35 USC § 112, 1st paragraph for allegedly failing to comply with the written description requirement. The Patent Office contends that the applicants have failed to properly describe which domains of the claimed sequences must be conserved or conservatively mutated to maintain the

activity of the full sequences. The applicants respectfully traverse the rejection and request reconsideration in view of the following remarks.

The test for determining compliance with the written description requirement is whether the disclosure of the application as originally filed reasonably conveys to the artisan that the inventor has possession at the time of the later claimed subject matter. See *Chiron v Genentech*, 363 F3d 1247 (Fed Cir 2004) and *In re Alton*, 76 F.3d 1168, 1172 (Fed. Cir. 1996). The Examiner cites Example 11 of the Written Description Guidelines published March 25, 2008, (hereinafter "the Guidelines"), as evidence of the alleged lack of written description of the claims in the specification. Example 11 relates to claims for a polynucleotide encoding a polypeptide having a recited percent identity to a known polypeptide sequence, further wherein the polypeptide has a recited activity. Example 11A discusses a claim for a polynucleotide encoding a polypeptide having 85% identity to a polypeptide and having a recited activity. The polypeptide in Example 11A has no known sequence identity to any other polypeptide or polypeptide family. The Guidelines state that one of ordinary skill can readily obtain sequences that are 85% identical to the known sequence due to the high level of skill in the art, but states that because there is no known correlation between the structure of the polypeptide sequence and its function there is no written description for a polypeptide having 85% identity to the identified polypeptide and having a recited activity. The examiner asserts that the present situation is analogous to Example 11A and therefore the claim lacks written description in the specification.

The claims presented herein are akin to Example 11B in the Guidelines. Example 11B relates to a polynucleotide encoding a polypeptide at least 85% identical to a known polypeptide sequence and having a recited activity. In this example, the specification does not disclose which of the nucleic acid (or amino acid) residues that encode a polypeptide having 85% identity to the known sequence can be changed and the polypeptide still retain the stated activity Y. The specification in the example identifies two domains of the polypeptide responsible for activity Y, i.e., a binding domain and a catalytic domain. In Example 11B, the specification states that it is expected that a polypeptide having a conservative substitution should retain

the stated activity, but the example goes on to note that "all conservative substitutions in these domains will not necessarily result in a protein having activity Y, but one of ordinary skill in the art would expect that many of these conservative substitutions would result in a protein having the required activity." Based on this analysis, the Guidelines consider that there is an adequate structure-function correlation since particular domains of the polypeptide are disclosed in specification, and those of ordinary skill would conclude that the applicant would have been in possession of the claimed genus of polynucleotides and polypeptides. Thus, the claims directed to a polynucleotide encoding a polypeptide having at least 85% identity to a known sequence and retaining a recited activity is adequately described. Example 11B is similar to the situation in the present application.

As stated in the Guidelines, it is well within the ability of one of ordinary skill to take the nucleic acid sequence of SEQ ID NO: 1 or 2 and envisage the chemical structure of any nucleic acid having a recited percent identity, e.g., 90%, to the recited nucleic acids. Thus, based on the description in the specification and knowledge in the art, it is clear that one of ordinary skill is in possession of the chemical structure of a nucleic acid 90% identical to the sequence of SEQ ID NO: 1 or 2, and would understand that the inventors were in possession of said nucleic acids at the time of filing.

The Patent Office has failed to properly consider the teaching of the Applicants' specification (and specifically identified in the applicants' response of November 20, 2008) with respect to identification of the portions of SEQ ID NO: 1 and 2 that are important for the recited activity. In the specification, the applicants have identified a core sequence of SEQ ID NO: 1 and 2 (SEQ ID NO: 3) and have provided experimental results for SEQ ID NO: 4, which comprises the core sequence of SEQ ID NO: 3 and is a truncated mutant of SEQ ID NO: 2. Moreover, the applicants have further provided that mutations to introduce unnatural nucleosides can be performed in order to increase stability of the resulting aptamer. For example, the applicants prepared sequence wherein the pyrimidine nucleotides U and C were replaced with analogs where the hydroxyl group (i.e., –OH) of the nucleotide was substituted by an amino group (i.e., $-NH_2$) instead. This substitution

results in a nucleoside having increased stability towards nuclease degradation (see specification at p. 5, lines 20-23). Additionally, the applicants have identified a portion of the SEQ ID NO: 2 that is important to activity (helix H1). The portion of the sequence which has been identified as important to activity accounts for over 40% of the entire sequence of SEQ ID NO: 2 (see 28 nucleobase sequence of SEQ ID NO: 2, identified on page 8, line 24 of specification, which corresponds to Helix H1 of Figure 1). The flanking F helix was shown to be less important. In the interest of furthering prosecution, the applicants have amended claim 1 to recite that the sequence must have at least 90% identity to that of SEQ ID NO: 1 or 2. The applicants have provided five examples of sequences (SEQ ID NO: 1-5) within this class that conserve the anti-apoptotic activity or are predicted to conserve anti-apoptotic activity. Thus, the plethora of guidance provided in the specification as to where conservative mutations or no mutations can exist (i.e., at Helix H1) and where other types of mutations may be tolerated (i.e., at least at Helix F), affords the skilled artisan with sufficient understanding on how to proceed in making the 10% variants recited in claim 1 to arrive at nucleic acids having anti-apoptotic activity. As noted in Example 11B, not all substitutions to SEQ ID NO: 1 and 2 within the recited percent identity will necessarily result in nucleic acids having the recited activity, but that does not preclude a finding that the written description requirements have been met.

As evidenced above, the nucleic acids described herein are described in detail similar to that provided for Example 11B in the Written Description Guidelines, in that the nucleic acid motifs are identified, as in Example 11B of the Guidelines the catalytic and binding domains are identified. As such, one of the ordinary skill would understand that the inventors were in possession of the claimed genus of nucleic acids which are at least 90% identical to SEQ ID NO: 1 and 2 and which have anti-apoptotic activity, at the time of filing the application.

THE REJECTION OF CLAIMS 11 AND 12 UNDER 35 USC § 112 ARE MOOT

With this paper, the applicants have canceled claims 11 and 12. Thus, this rejection is moot and should be withdrawn.

THE REJECTION OF CLAIMS 13 AND 18-20 UNDER 35 USC § 102 SHOULD BE WITHDRAWN

With this paper, the applicants have amended claims 13 and 18-20 as suggested by the examiner to properly address this rejection. It is submitted that this rejection therefore should be withdrawn.

CONCLUSION

In view of the above amendments and remarks, the applicants believe that this application is in condition for allowance. Should the examiner wish to discuss the foregoing or any matter of form in an effort to advance this application toward allowance, he is urged to telephone the undersigned at the indicated number.

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Respectfully submitted,

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